

w/ #6A

-1-

SEQUENCE LISTING

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A22



<110> Hanke, Paul D.

Li-D'Elia, Lhing-Yew

Rayapati, John

Crafton, Corey

Walsh, Holly

<120> Increased Lysine Production by Gene Amplification

<130> 1533.1030002

<140> 09/722,441

<141> 2000-11-28

<150> US 60/173,707

<151> 1999-12-30

<150> US 60/184,130

<151> 2000-02-22

<160> 37

<170> PatentIn version 3.0

<210> 1

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

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gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct 96
 Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
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gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat 144
 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt 192
 Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60

gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc 240
 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80

gtc gcc atg gct att gag tcc ctt ggc gca gaa gct caa tct ttc act 288
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95

ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc 336
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110

att gtt gac gtc aca ccg ggt cgt gtg cgt gaa gca ctc gat gag ggc 384
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125

aag atc tgc att gtt gct ggt ttt cag ggt gtt aat aaa gaa acc cgc 432
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140

gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg 480
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160

ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt 528
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 165 170 175

gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag 576
 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190

ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc 624
 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205

tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat 672
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220

gtg cca ctt cgc gta cgc tcg tct tat agt aat gat ccc ggc act ttg 720
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240

att gcc ggc tct atg gag gat att cct gtg gaa gaa gca gtc ctt acc 768
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr

245										250					255					
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tcc	gat	aag	cca	ggc	gag	gct	gcc	aag	gtt	ttc	cgt	gcg	ttg	gct	gat	864				
Ser	Asp	Lys	Pro	Gly	Glu	Ala	Ala	Lys	Val	Phe	Arg	Ala	Leu	Ala	Asp					
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gca	gaa	atc	aac	att	gac	atg	gtt	ctg	cag	aac	gtc	tcc	tct	gtg	gaa	912				
Ala	Glu	Ile	Asn	Ile	Asp	Met	Val	Leu	Gln	Asn	Val	Ser	Ser	Val	Glu					
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gac	ggc	acc	acc	gac	atc	acg	ttc	acc	tgc	cct	cgc	gct	gac	gga	cgc	960				
Asp	Gly	Thr	Thr	Asp	Ile	Thr	Phe	Thr	Cys	Pro	Arg	Ala	Asp	Gly	Arg					
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cgt	gcg	atg	gag	atc	ttg	aag	aag	ctt	cag	gtt	cag	ggc	aac	tgg	acc	1008				
Arg	Ala	Met	Glu	Ile	Leu	Lys	Lys	Leu	Gln	Val	Gln	Gly	Asn	Trp	Thr					
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aat	gtg	ctt	tac	gac	gac	cag	gtc	ggc	aaa	gtc	tcc	ctc	gtg	ggt	gct	1056				
Asn	Val	Leu	Tyr	Asp	Asp	Gln	Val	Gly	Lys	Val	Ser	Leu	Val	Gly	Ala					
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ggc	atg	aag	tct	cac	cca	ggt	gtt	acc	gca	gag	ttc	atg	gaa	gct	ctg	1104				
Gly	Met	Lys	Ser	His	Pro	Gly	Val	Thr	Ala	Glu	Phe	Met	Glu	Ala	Leu					
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cgc	gat	gtc	aac	gtg	aac	atc	gaa	ttg	att	tcc	atc	tct	gag	atc	cgc	1152				
Arg	Asp	Val	Asn	Val	Asn	Ile	Glu	Leu	Ile	Ser	Ile	Ser	Glu	Ile	Arg					
	370					375					380									
att	tcc	gtg	ctg	atc	cgt	gaa	gat	gat	ctg	gat	gct	gct	gca	cg	gca	1200				
Ile	Ser	Val	Leu	Ile	Arg	Glu	Asp	Asp	Leu	Asp	Ala	Ala	Ala	Arg	Ala					
	385				390					395					400					
ttg	cat	gag	cag	ttc	cag	ctg	ggc	ggc	gaa	gac	gaa	gcc	gtc	gtt	tat	1248				
Leu	His	Glu	Gln	Phe	Gln	Leu	Gly	Gly	Glu	Asp	Glu	Ala	Val	Val	Tyr					
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gca	ggc	acc	gga	cg	taa											1266				
Ala	Gly	Thr	Gly	Arg																
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<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

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Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
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Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
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Ala Gly Thr Gly Arg
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atg cgc acc ttt ttg gaa gag cgc aat ttc cca gct gac act gtt cgt Met Arg Thr Phe Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg	20	25	30	96
ttc ttt gct tcc ccg cgt tcc gca ggc cgt aag att gaa ttc cgt ggc Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly	35	40	45	144
acg gaa atc gag gta gaa gac att act cag gca acc gag gag tcc ctc Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu	50	55	60	192
aag ggc atc gac gtt gcg ttg ttc tct gct gga ggc acc gct tcc aag Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys	65	70	75	240
cag tac gct cca ctg ttt gct gct gca ggc gcg act gtt gtg gat aac Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn	85	90	95	288
tct tct gct tgg cgc aag gac gac gag gtt cca cta atc gtc tct gag Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu	100	105	110	336
gtg aac cct tcc gac aag gat tcc ctg gtc aag ggc att att gcg aat Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn	115	120	125	384
cct aac tgc acc acc atg gct gca atg cca gtg ctg aag cca ctg cac Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His	130	135	140	432
gat gcc gct ggt ctt gta aag ctt cac gtt tcc tct tac cag gct gtt Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val	145	150	155	480
tcc ggt tct ggt ctt gca ggt gtg gaa acc ttg gca aag cag gtt gct Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala	165	170	175	528
gca gtt ggc gac cac aac gtt gag ttc gtc cat gat gga cag gct gct Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala	180	185	190	576
gac gca ggc gat gtc gga cct tac gtt tcc cca atc gct tac aac gtg Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val	195	200	205	624
ctg cca ttc gcc gga aac ctc gtc gat gac ggc acc ttc gaa acc gac Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp	210	215	220	672
gaa gag cag aag ctg cgc aac gaa tcc cgc aag att ctc ggc ctc cca Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro	225	230	235	720
gac ctc aag gtc tca ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc Asp Leu Lys Val Ser Thr Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly	245	250	255	768

cac acg ctg acc att cac gcc gaa ttc gac aag gca atc acc gtc gag 816
His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu
260 265 270

cag gcg cag gag atc ttg ggt gcc gct tca ggc gtc gag ctt gtc gac 864
Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp
275 280 285

gtc cca acc cca ctt gca gct gcc ggc att gac gaa tcc ctc gtt gga 912
Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
290 295 300

cgc atc cgt cag gac tcc act gtc gac gac aac cgc ggt ctg gtt ctc 960
Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu
305 310 315 320

gtc gta tct ggc gat aac ctt cgc aag ggc gca gca ctg aac acc att 1008
Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile
325 330 335

cag att gct gag ctg ctg gtt aag taa 1035
Gln Ile Ala Glu Leu Leu Val Lys
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<211> 344

<212> PRT

<213> Corynebacterium glutamicum

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Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly
35 40 45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
50 55 60

Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
65 70 75 80

Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn
85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu

100	105	110
Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn 115 120 125		
Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His 130 135 140		
Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val 145 150 155 160		
Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala 165 170 175		
Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala 180 185 190		
Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val 195 200 205		
Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp 210 215 220		
Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro 225 230 235 240		
Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly 245 250 255		
His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu 260 265 270		
Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp 275 280 285		
Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly 290 295 300		
Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu 305 310 315 320		
Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile 325 330 335		
Gln Ile Ala Glu Leu Leu Val Lys 340		

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<212> DNA

<213> Corynebacterium glutamicum

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ggt gga gta gca atg gtt act cca ttc acg gaa tcc gga gac atc gat	96
Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp	
20 25 30	

atc gct gct ggc cgc gaa gtc gcg gct tat ttg gtt gat aag ggc ttg	144
Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu	
35 40 45	

gat tct ttg gtt ctc gcg ggc acc act ggt gaa tcc cca acg aca acc	192
Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr	
50 55 60	

gcc gct gaa aaa cta gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg	240
Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly	
65 70 75 80	

gat cgg gcg aag ctc atc gcc ggt gtc gga acc aac aac acg cgg aca	288
Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr	
85 90 95	

tct gtg gaa ctt gcg gaa gct gct gct tct gct ggc gca gac ggc ctt	336
Ser Val Glu Leu Ala Glu Ala Ala Ser Ala Gly Ala Asp Gly Leu	
100 105 110	

tta gtt gta act cct tat tac tcc aag ccg agc caa gag gga ttg ctg	384
Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu	
115 120 125	

gcg cac ttc ggt gca att gct gca gca aca gag gtt cca att tgt ctc	432
Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu	
130 135 140	

tat gac att cct ggt cgg tca ggt att cca att gaa tct gat acc atg	480
Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met	
145 150 155 160	

aga cgc ctg agt gaa tta cct acg att ttg gcg gtc aag gac gcc aag	528
Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys	
165 170 175	

ggt gac ctc gtt gca gcc acg tca ttg atc aaa gaa acg gga ctt gcc 576
 Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
 180 185 190

tgg tat tca ggc gat gac cca cta aac ctt gtt tgg ctt gct ttg ggc 624
 Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
 195 200 205

gga tca ggt ttc att tcc gta att gga cat gca gcc ccc aca gca tta 672
 Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
 210 215 220

cgt gag ttg tac aca agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg 720
 Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
 225 230 235 240

gaa atc aac gcc aaa cta tca ccg ctg gta gct gcc caa ggt cgc ttg 768
 Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
 245 250 255

ggt gga gtc agc ttg gca aaa gct gct ctg cgt ctg cag ggc atc aac 816
 Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn
 260 265 270

gta gga gat cct cga ctt cca att atg gct cca aat gag cag gaa ctt 864
 Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
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<210> 6

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

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Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
 35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
 50 55 60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly
 65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu
100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
115 120 125

Ala His Phe Gly Ala Ile Ala Ala Thr Glu Val Pro Ile Cys Leu
130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn
260 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
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Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu
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<212> DNA

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<222> (1)..(747)

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Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala	
20 25 30	
gag atc ggc gtc gac gat gat ttg agc ctt ctg gta gac aac ggc gct	144
Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala	
35 40 45	
gaa gtt gtc gtt gac ttc acc act cct aac gct gtg atg ggc aac ctg	192
Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu	
50 55 60	
gag ttc tgc atc aac aac ggc att tct gcg gtt gtt gga acc acg ggc	240
Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly	
65 70 75 80	
ttc gat aat gct cgt ttg gag cag gtt cgc gcc tgg ctt gaa gga aaa	288
Phe Asp Asn Ala Arg Leu Glu Gln Val Arg Ala Trp Leu Glu Gly Lys	
85 90 95	
gac aat gtc ggt gtt ctg atc gca cct aac ttt gct atc tct gcg gtg	336
Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val	
100 105 110	
ttg acc atg gtc ttt tcc aag cag gct gcc cgc ttc ttc gaa tca gct	384
Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala	
115 120 125	
gaa gtt att gag ctg cac cac ccc aac aag ctg gat gca cct tca ggc	432
Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly	
130 135 140	
acc gcg atc cac act gct cag ggc att gct gcg gca cgc aaa gaa gca	480
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala	
145 150 155 160	
ggc atg gac gca cag cca gat gcg acc gag cag gca ctt gag ggt tcc	528
Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser	
165 170 175	
cgt ggc gca agc gta gat gga atc cca gtt cac gca gtc cgc atg tcc	576
Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser	
180 185 190	

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ggc atg gtt gct cac gag caa gtt atc ttt ggc acc cag ggt cag acc      624
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ttg acc atc aag cag gac tcc tat gat cgc aac tca ttt gca cca ggt      672
Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
      210                215                220

gtc ttg gtg ggt gtg cgc aac att gca cag cac cca ggc cta gtc gta      720
Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
      225                230                235                240

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Gly Leu Glu His Tyr Leu Gly Leu
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<210> 8

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

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Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
      35      40      45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
      50      55      60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
      65      70      75      80

Phe Asp Asn Ala Arg Leu Glu Gln Val Arg Ala Trp Leu Glu Gly Lys
      85      90      95

Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
      100      105      110

Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
      115      120      125

Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly

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130		135		140
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala				
145		150		155
Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser				
		165		170
				175
Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser				
		180		185
				190
Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr				
		195		200
				205
Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly				
		210		215
				220
Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val				
		225		230
				235
				240
Gly Leu Glu His Tyr Leu Gly Leu				
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<210> 9

<211> 1023

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(1023)

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gat tac aag aac atg acc aac atc cgc gta gct atc gta ggc tac gga	96
Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly	
20 25 30	
aac ctg gga cgc agc gtc gaa aag ctt att gcc aag cag ccc gac atg	144
Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met	
35 40 45	
gac ctt gta gga atc ttc tcg cgc cgg gcc acc ctc gac aca aag acg	192

Asp	Leu	Val	Gly	Ile	Phe	Ser	Arg	Arg	Ala	Thr	Leu	Asp	Thr	Lys	Thr	
50						55					60					
cca	gtc	ttt	gat	gtc	gcc	gac	gtg	gac	aag	cac	gcc	gac	gac	gtg	gac	240
Pro	Val	Phe	Asp	Val	Ala	Asp	Val	Asp	Lys	His	Ala	Asp	Asp	Val	Asp	
65					70					75					80	
gtg	ctg	ttc	ctg	tgc	atg	ggc	tcc	gcc	acc	gac	atc	cct	gag	cag	gca	288
Val	Leu	Phe	Leu	Cys	Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	
				85					90					95		
cca	aag	ttc	gcg	cag	ttc	gcc	tgc	acc	gta	gac	acc	tac	gac	aac	cac	336
Pro	Lys	Phe	Ala	Gln	Phe	Ala	Cys	Thr	Val	Asp	Thr	Tyr	Asp	Asn	His	
			100					105					110			
cgc	gac	atc	cca	cgc	cac	cgc	cag	gtc	atg	aac	gaa	gcc	gcc	acc	gca	384
Arg	Asp	Ile	Pro	Arg	His	Arg	Gln	Val	Met	Asn	Glu	Ala	Ala	Thr	Ala	
		115					120					125				
gcc	ggc	aac	gtt	gca	ctg	gtc	tct	acc	ggc	tgg	gat	cca	gga	atg	ttc	432
Ala	Gly	Asn	Val	Ala	Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	
	130					135					140					
tcc	atc	aac	cgc	gtc	tac	gca	gcg	gca	gtc	tta	gcc	gag	cac	cag	cag	480
Ser	Ile	Asn	Arg	Val	Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	
	145				150					155					160	
cac	acc	ttc	tgg	ggc	cca	ggt	ttg	tca	cag	ggc	cac	tcc	gat	gct	ttg	528
His	Thr	Phe	Trp	Gly	Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	
				165					170					175		
cga	cgc	atc	cct	ggc	gtt	caa	aag	gcc	gtc	cag	tac	acc	ctc	cca	tcc	576
Arg	Arg	Ile	Pro	Gly	Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	
			180					185					190			
gaa	gaa	gcc	ctg	gaa	aag	gcc	cgc	cgt	ggc	gaa	gcc	ggc	gac	ctc	acc	624
Glu	Glu	Ala	Leu	Glu	Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	
		195					200					205				
gga	aag	caa	acc	cac	aag	cgc	caa	tgc	ttc	gtg	gtt	gcc	gac	gcg	gcc	672
Gly	Lys	Gln	Thr	His	Lys	Arg	Gln	Cys	Phe	Val	Val	Ala	Asp	Ala	Ala	
	210					215					220					
gac	cac	gag	cgc	atc	gaa	aac	gac	atc	cgc	acc	atg	cct	gat	tac	ttc	720
Asp	His	Glu	Arg	Ile	Glu	Asn	Asp	Ile	Arg	Thr	Met	Pro	Asp	Tyr	Phe	
	225				230				235						240	
gtt	ggc	tac	gaa	gtc	gaa	gtc	aac	ttc	atc	gac	gaa	gca	acc	ttg	gac	768
Val	Gly	Tyr	Glu	Val	Glu	Val	Asn	Phe	Ile	Asp	Glu	Ala	Thr	Leu	Asp	
				245					250					255		
gcc	gag	cac	acc	ggc	atg	cca	cac	ggc	gga	cac	gtg	atc	acc	acc	ggc	816
Ala	Glu	His	Thr	Gly	Met	Pro	His	Gly	Gly	His	Val	Ile	Thr	Thr	Gly	
			260					265					270			
gac	acc	ggt	ggc	ttc	aac	cac	acc	gtg	gaa	tac	atc	ctg	aag	ctg	gac	864
Asp	Thr	Gly	Gly	Phe	Asn	His	Thr	Val	Glu	Tyr	Ile	Leu	Lys	Leu	Asp	
		275					280					285				
cga	aac	cca	gat	ttc	acc	gct	tct	tca	cag	atc	gct	ttc	ggc	cgc	gca	912
Arg	Asn	Pro	Asp	Phe	Thr	Ala	Ser	Ser	Gln	Ile	Ala	Phe	Gly	Arg	Ala	
	290					295					300					

gct cac cgc atg aag cag cag ggc caa agc ggt gct ttc acc gtc ctc 960
Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
305 310 315 320

gaa gtt gct cca tac ttg ctc tcc ccg gag aac ttg gat gat ctg atc 1008
Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
325 330 335

gca cgc gac gtc taa 1023
Ala Arg Asp Val
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<210> 10

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

Met His Phe Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
1 5 10 15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
20 25 30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
165 170 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
180 185 190

Glu Glu Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
210 215 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
225 230 235 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Leu Asp
245 250 255

Ala Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
260 265 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
275 280 285

Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
290 295 300

Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
305 310 315 320

Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
325 330 335

Ala Arg Asp Val
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<211> 1338

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(1338)

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Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro	
1 5 10 15	
cgc aat gca gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg	96
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val	
20 25 30	
cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc	144
Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val	
35 40 45	
gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc	192
Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe	
50 55 60	
ggt gga cca ggc aat gtg cac tac gca tcc aaa gcg ttc ctg acc aag	240
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys	
65 70 75 80	
acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gcg	288
Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala	
85 90 95	
tcc atc aat gaa ctg ggc att gcc ctg gcc gct ggt ttc ccg gcc agc	336
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser	
100 105 110	
cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg	384
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala	
115 120 125	
ttg gtt caa aac ggt gtc ggg cat gtg gtg ctg gac tcc gcg cag gaa	432
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu	
130 135 140	
ttg gaa ctg ctg gat tac gtt gcc gct ggt gaa ggc aag atc cag gac	480
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp	
145 150 155 160	
gtg ttg atc cgc gtg aag cca ggt atc gaa gcc cac acc cac gag ttc	528
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe	
165 170 175	
atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc	576
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser	
180 185 190	
ggt tcc gca ttc gaa gca gcg aaa gca gcc aac aat gca gag aac ttg	624
Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu	
195 200 205	
aac ctg gtt ggt ctg cac tgc cat gtt ggt tcc cag gtg ttc gac gcc	672
Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala	
210 215 220	

gaa ggc ttc aag ctg gca gca gag cgc gtg ttg ggc ctg tac tca cag Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln 225 230 235 240	720
atc cac agc gaa cta ggt gtc gcc ctt cct gag ctg gac ctc ggt ggc Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly 245 250 255	768
gga tac ggc atc gcc tac act gca gat gag gaa cca ctc aac gtc gca Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala 260 265 270	816
gaa gtc gcc tcc gac cta ctc acc gca gtc gga aaa atg gca gcg gaa Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu 275 280 285	864
cta ggc atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile 290 295 300	912
gca ggc ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa aac Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asn 305 310 315 320	960
gtc cac gta gac gac gac aaa acc cgc cgc tac gta gcc gtc gac gga Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Val Ala Val Asp Gly 325 330 335	1008
ggc atg tcc gac aac atc cgc cca gca ctc tac ggc tcc gaa tac gac Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp 340 345 350	1056
gcc cgc gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg 355 360 365	1104
atc gtg ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu 370 375 380	1152
atc tac cca tct gac atc acc agc ggc gac ttc ctc gca ctc gca gcc Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala 385 390 395 400	1200
acc ggc gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr 405 410 415	1248
cgg ccc gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu 420 425 430	1296
cgc cgc gaa acc ctc gac gac atc ctc tca cta gag gca taa Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala 435 440 445	1338

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<211> 445

<212> PRT

<213> Corynebacterium glutamicum

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20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu
195 200 205

Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
225 230 235 240

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
245 250 255

Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala
260 265 270

Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu
275 280 285

Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile
290 295 300

Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asn
305 310 315 320

Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Val Ala Val Asp Gly
325 330 335

Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp
340 345 350

Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg
355 360 365

Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu
370 375 380

Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala
385 390 395 400

Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr
405 410 415

Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu
420 425 430

Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
435 440 445

<210> 13

<211> 1338

<212> DNA

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<220>

<221> CDS

<222> (1)..(1338)

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Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro	
1 5 10 15	
cgc aat gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg	96
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val	
20 25 30	
cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc	144
Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val	
35 40 45	
gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc	192
Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe	
50 55 60	
ggt gga cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag	240
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys	
65 70 75 80	
acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca	288
Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala	
85 90 95	
tcc atc aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc	336
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser	
100 105 110	
cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg	384
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala	
115 120 125	
ttg gtt caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa	432
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu	
130 135 140	
cta gaa ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac	480
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp	
145 150 155 160	
gtg ttg atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc	528
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe	
165 170 175	
atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc	576
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser	
180 185 190	
ggt tcc gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg	624

Gly	Ser	Ala	Phe	Glu	Ala	Ala	Lys	Ala	Ala	Asn	Asn	Ala	Glu	Asn	Leu	
		195					200					205				
aac	ctg	ggt	ggc	ctg	cac	tgc	cac	ggt	ggt	tcc	cag	gtg	ttc	gac	gcc	672
Asn	Leu	Val	Gly	Leu	His	Cys	His	Val	Gly	Ser	Gln	Val	Phe	Asp	Ala	
	210					215					220					
gaa	ggc	ttc	aag	ctg	gca	gca	gaa	cgc	gtg	ttg	ggc	ctg	tac	tca	cag	720
Glu	Gly	Phe	Lys	Leu	Ala	Ala	Glu	Arg	Val	Leu	Gly	Leu	Tyr	Ser	Gln	
225					230					235					240	
atc	cac	agc	gaa	ctg	ggc	ggt	gcc	ctt	cct	gaa	ctg	gat	ctc	ggt	ggc	768
Ile	His	Ser	Glu	Leu	Gly	Val	Ala	Leu	Pro	Glu	Leu	Asp	Leu	Gly	Gly	
			245						250					255		
gga	tac	ggc	att	gcc	tat	acc	gca	gct	gaa	gaa	cca	ctc	aac	gtc	gca	816
Gly	Tyr	Gly	Ile	Ala	Tyr	Thr	Ala	Ala	Glu	Glu	Pro	Leu	Asn	Val	Ala	
			260				265						270			
gaa	ggt	ggc	tcc	gac	ctg	ctc	acc	gca	gtc	gga	aaa	atg	gca	gcg	gaa	864
Glu	Val	Ala	Ser	Asp	Leu	Leu	Thr	Ala	Val	Gly	Lys	Met	Ala	Ala	Glu	
	275						280					285				
cta	ggc	atc	gac	gca	cca	acc	gtg	ctt	ggt	gag	ccc	ggc	cgc	gct	atc	912
Leu	Gly	Ile	Asp	Ala	Pro	Thr	Val	Leu	Val	Glu	Pro	Gly	Arg	Ala	Ile	
	290					295					300					
gca	ggc	ccc	tcc	acc	gtg	acc	atc	tac	gaa	gtc	ggc	acc	acc	aaa	gac	960
Ala	Gly	Pro	Ser	Thr	Val	Thr	Ile	Tyr	Glu	Val	Gly	Thr	Thr	Lys	Asp	
305					310					315					320	
gtc	cac	gta	gac	gac	gac	aaa	acc	cgc	cgt	tac	atc	gcc	gtg	gac	gga	1008
Val	His	Val	Asp	Asp	Asp	Lys	Thr	Arg	Arg	Tyr	Ile	Ala	Val	Asp	Gly	
			325						330					335		
ggc	atg	tcc	gac	aac	atc	cgc	cca	gca	ctc	tac	ggc	tcc	gaa	tac	gac	1056
Gly	Met	Ser	Asp	Asn	Ile	Arg	Pro	Ala	Leu	Tyr	Gly	Ser	Glu	Tyr	Asp	
			340				345						350			
gcc	cgc	gta	gta	tcc	cgc	ttc	gcc	gaa	gga	gac	cca	gta	agc	acc	cgc	1104
Ala	Arg	Val	Val	Ser	Arg	Phe	Ala	Glu	Gly	Asp	Pro	Val	Ser	Thr	Arg	
		355				360						365				
atc	gtg	ggc	tcc	cac	tgc	gaa	tcc	ggc	gat	atc	ctg	atc	aac	gat	gaa	1152
Ile	Val	Gly	Ser	His	Cys	Glu	Ser	Gly	Asp	Ile	Leu	Ile	Asn	Asp	Glu	
	370					375					380					
atc	tac	cca	tct	gac	atc	acc	agc	ggc	gac	ttc	ctt	gca	ctc	gca	gcc	1200
Ile	Tyr	Pro	Ser	Asp	Ile	Thr	Ser	Gly	Asp	Phe	Leu	Ala	Leu	Ala	Ala	
385					390					395					400	
acc	ggc	gca	tac	tgc	tac	gcc	atg	agc	tcc	cgc	tac	aac	gcc	ttc	aca	1248
Thr	Gly	Ala	Tyr	Cys	Tyr	Ala	Met	Ser	Ser	Arg	Tyr	Asn	Ala	Phe	Thr	
				405					410					415		
cgg	ccc	ggc	gtc	gtg	tcc	gtc	cgc	gct	ggc	agc	tcc	cgc	ctc	atg	ctg	1296
Arg	Pro	Ala	Val	Val	Ser	Val	Arg	Ala	Gly	Ser	Ser	Arg	Leu	Met	Leu	
			420					425					430			
cgc	cgc	gaa	acg	ctc	gac	gac	atc	ctc	tca	cta	gag	gca	taa			1338
Arg	Arg	Glu	Thr	Leu	Asp	Asp	Ile	Leu	Ser	Leu	Glu	Ala				
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<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
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Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val
20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu

195	200	205
Asn 210	Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala 215	220
Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln 225	230	235 240
Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly 245	250	255
Gly Tyr Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala 260	265	270
Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu 275	280	285
Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile 290	295	300
Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp 305	310	315 320
Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly 325	330	335
Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp 340	345	350
Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg 355	360	365
Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu 370	375	380
Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala 385	390	395 400
Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr 405	410	415
Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu 420	425	430
Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala 435	440	445

<210> 15

<211> 753

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(753)

<400> 15

gtg gcc gaa caa gtt aaa ttg agc gtg gag ttg ata gcg tgc agt tct	48
Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser	
1 5 10 15	

ttt act cca ccc gct gat gtt gag tgg tca act gat gtt gag ggc gcg	96
Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala	
20 25 30	

gaa gca ctc gtc gag ttt gcg ggt cgt gcc tgc tac gaa act ttt gat	144
Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp	
35 40 45	

aag ccg aac cct cga act gct tcc aat gct gcg tat ctg cgc cac atc	192
Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile	
50 55 60	

atg gaa gtg ggg cac act gct ttg ctt gag cat gcc aat gcc acg atg	240
Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met	
65 70 75 80	

tat atc cga ggc att tct cgg tcc gcg acc cat gaa ttg gtc cga cac	288
Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His	
85 90 95	

cgc cat ttt tcc ttc tct caa ctg tct cag cgt ttc gtg cac agc gga	336
Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly	
100 105 110	

gaa tcg gaa gta gtg gtg ccc act ctc atc gat gaa gat ccg cag ttg	384
Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu	
115 120 125	

cgt gaa ctt ttc atg cac gcc atg gat gag tct cgg ttc gct ttc aat	432
Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn	
130 135 140	

gag ctg ctt aat gcg ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca	480
Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala	
145 150 155 160	

ctt tta agg aaa aag cag gct cgt caa gca gct cgc gct gtg ctg ccc	528
Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro	
165 170 175	

aac gct aca gag tcc aga atc gtg gtg tct gga aac ttc cgc acc tgg 576
Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp
180 185 190

agg cat ttc att ggc atg cga gcc agt gaa cat gca gac gtc gaa atc 624
Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile
195 200 205

cgc gaa gta gcg gta gga tgt tta aga aag ctg cag gta gca gcg cca 672
Arg Glu Val Ala Val Gly Cys Leu Arg Lys Leu Gln Val Ala Ala Pro
210 215 220

act gtt ttc ggt gat ttt gag att gaa act ttg gca gac gga tcg caa 720
Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln
225 230 235 240

atg gca aca agc ccg tat gtc atg gac ttt taa 753
Met Ala Thr Ser Pro Tyr Val Met Asp Phe
245 250

<210> 16

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
1 5 10 15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu

115 120 125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn
130 135 140

Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala
145 150 155 160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro
165 170 175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp
180 185 190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile
195 200 205

Arg Glu Val Ala Val Gly Cys Leu Arg Lys Leu Gln Val Ala Ala Pro
210 215 220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln
225 230 235 240

Met Ala Thr Ser Pro Tyr Val Met Asp Phe
245 250

<210> 17

<211> 551

<212> DNA

<213> *Corynebacterium glutamicum*

<400> 17

aaccggtgtg gagccgacca ttccgcgagg ctgcactgca acgaggtcgt agtttttggtta 60

catggcttct ggccagttca tggattggct gccgaagaag ctataggcat cgccaccagg 120

gccaccggag ttaccgaaga tggtgccgtg cttttcgctt tgggcaggga ccttgacaaa 180

gcccacgctg atatcgccaa gtgagggatc agaatagtgc atgggcacgt cgatgctgcc 240

acattgagcg gaggcaatat ctacctgagg tgggcattct tcccagcgga tgttttcttg 300

cgctgctgca gtgggcattg ataccaaaaa ggggctaagc gcagtcgagg cggaagaac 360

tgctactacc ttttttattg tcgaacgggg cattacggct ccaaggacgt ttgttttctg 420

ggtcagttac cccaaaaagc atatacagag accaatgatt tttcattaaa aaggcaggga 480

tttggtataa gtatgggtcg tattctgtgc gacgggtgta cctcggctag aatttctccc 540

catgacacca g

551

<210> 18

<211> 365

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(365)

<400> 18

gtg gcc gaa caa gtt aaa ttg agc gtg gag ttg ata gcg tgc agt tct	48
Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser	
1 5 10 15	

ttt act cca ccc gct gat gtt gag tgg tca act gat gtt gag ggc gcg	96
Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala	
20 25 30	

gaa gca ctc gtc gag ttt gcg ggt cgt gcc tgc tac gaa act ttt gat	144
Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp	
35 40 45	

aag ccg aac cct cga act gct tcc aat gct gcg tat ctg cgc cac atc	192
Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile	
50 55 60	

atg gaa gtg ggg cac act gct ttg ctt gag cat gcc aat gcc acg atg	240
Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met	
65 70 75 80	

tat atc cga ggc att tct cgg tcc gcg acc cat gaa ttg gtc cga cac	288
Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His	
85 90 95	

cgc cat ttt tcc ttc tct caa ctg tct cag cgt ttc gtg cac agc gga	336
Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly	
100 105 110	

gaa tcg gaa gta gtg gtg ccc act ctc at	365
Glu Ser Glu Val Val Val Pro Thr Leu Ile	
115 120	

<210> 19

<211> 122

<212> PRT

<213> Corynebacterium glutamicum

<400> 19

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
1 5 10 15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile
115 120

<210> 20

<211> 833

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(833)

<400> 20

atg gct aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca 48
Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
1 5 10 15

cgc aat gca gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg 96
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val
20 25 30

cct	ctg	cct	gac	ctc	gct	gaa	gaa	tac	gga	acc	cca	ctg	ttc	gta	gtc	144
Pro	Leu	Pro	Asp	Leu	Ala	Glu	Glu	Tyr	Gly	Thr	Pro	Leu	Phe	Val	Val	
35																192
gac	gag	gac	gat	ttc	cgt	tcc	cgc	tgt	cgc	gac	atg	gct	acc	gca	ttc	
Asp	Glu	Asp	Asp	Phe	Arg	Ser	Arg	Cys	Arg	Asp	Met	Ala	Thr	Ala	Phe	240
50																
ggt	gga	cca	ggc	aat	gtg	cac	tac	gca	tcc	aaa	gcg	ttc	ctg	acc	aag	288
Gly	Gly	Pro	Gly	Asn	Val	His	Tyr	Ala	Ser	Lys	Ala	Phe	Leu	Thr	Lys	
65																336
acc	att	gca	cgt	tgg	gtt	gat	gaa	gag	ggg	ctg	gca	ctg	gac	att	gcg	
Thr	Ile	Ala	Arg	Trp	Val	Asp	Glu	Glu	Gly	Leu	Ala	Leu	Asp	Ile	Ala	384
85																
tcc	atc	aat	gaa	ctg	ggc	att	gcc	ctg	gcc	gct	ggg	ttc	ccg	gcc	agc	432
Ser	Ile	Asn	Glu	Leu	Gly	Ile	Ala	Leu	Ala	Ala	Gly	Phe	Pro	Ala	Ser	
100																480
cgt	atc	acc	gcg	cac	ggc	aac	aac	aaa	ggc	gta	gag	ttc	ctg	gcg	gcg	
Arg	Ile	Thr	Ala	His	Gly	Asn	Asn	Lys	Gly	Val	Glu	Phe	Leu	Arg	Ala	528
115																
ttg	gtt	caa	aac	ggg	gtc	ggg	cat	gtg	gtg	ctg	gac	tcc	gcg	cag	gaa	576
Leu	Val	Gln	Asn	Gly	Val	Gly	His	Val	Val	Leu	Asp	Ser	Ala	Gln	Glu	
130																624
ttg	gaa	ctg	ctg	gat	tac	gtt	gcc	gct	ggg	gaa	ggc	aag	atc	cag	gac	
Leu	Glu	Leu	Leu	Asp	Tyr	Val	Ala	Ala	Gly	Glu	Gly	Lys	Ile	Gln	Asp	672
145																
gtg	ttg	atc	gcg	gtg	aag	cca	ggg	atc	gaa	gcc	cac	acc	cac	gag	ttc	720
Val	Leu	Ile	Arg	Val	Lys	Pro	Gly	Ile	Glu	Ala	His	Thr	His	Glu	Phe	
165																768
atc	gcc	act	agc	cac	gaa	gac	cag	aag	ttc	gga	ttc	tcc	ctg	gca	tcc	
Ile	Ala	Thr	Ser	His	Glu	Asp	Gln	Lys	Phe	Gly	Phe	Ser	Leu	Ala	Ser	816
180																
ggt	tcc	gca	ttc	gaa	gca	gcg	aaa	gca	gcc	aac	aat	gca	gag	aac	ttg	833
Gly	Ser	Ala	Phe	Glu	Ala	Ala	Lys	Ala	Ala	Asn	Asn	Ala	Glu	Asn	Leu	
195																888
aac	ctg	gtt	ggg	ctg	cac	tgc	cat	gtt	ggg	tcc	cag	gtg	ttc	gac	gcc	
Asn	Leu	Val	Gly	Leu	His	Cys	His	Val	Gly	Ser	Gln	Val	Phe	Asp	Ala	936
210																
gaa	ggc	ttc	aag	ctg	gca	gca	gag	cgc	gtg	ttg	ggc	ctg	tac	tca	cag	984
Glu	Gly	Phe	Lys	Leu	Ala	Ala	Glu	Arg	Val	Leu	Gly	Leu	Tyr	Ser	Gln	
225																1032
atc	cac	agc	gaa	cta	ggg	gtc	gcc	ctt	cct	gag	ctg	gac	ctc	ggg	ggc	
Ile	His	Ser	Glu	Leu	Gly	Val	Ala	Leu	Pro	Glu	Leu	Asp	Leu	Gly	Gly	1080
245																
gga	tac	ggc	atc	gcc	tac	act	gca	gat	gag	gaa	cca	ctc	aac	gtc	gca	1128
Gly	Tyr	Gly	Ile	Ala	Tyr	Thr	Ala	Asp	Glu	Glu	Pro	Leu	Asn	Val	Ala	
260																1176
gaa	gtc	gcc	tcc	gac	ct											
Glu	Val	Ala	Ser	Asp	Leu											1224
275																

<210> 21

<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 21

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
1 5 10 15

Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val
20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu
195 200 205

Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
 210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
 225 230 235 240

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
 245 250 255

Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala
 260 265 270

Glu Val Ala Ser Asp Leu
 275

<210> 22

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 22
 gggtagctcg cgaagtagca cctgtcac

28

<210> 23

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 23
 gcggatcccc catcgcccct caaaga

26

<210> 24

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 24
aacgggcggt gaagggaac t

21

<210> 25

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 25
tgaaagacag gggtatccag a

21

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 26
ccatggtacc aagtgcgtgg cgag

24

<210> 27

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 27

ccatggtacc acactgtttc cttgc 25

<210> 28

<211> 36

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 28

ctgggtccgg cgagtggagc cgaccattcc gcgagg 36

<210> 29

<211> 36

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 29

ctcgctccgg cgaggtcgga ggcaacttct gcgacg 36

<210> 30

<211> 6

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 30

ggtacc 6

<210> 31

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 31
ggatcttcac ctagatcc

18

<210> 32

<211> 16

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 32
ccctgataaa tgcttc

16

<210> 33

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 33
ccggagaaga tgtaacaatg gctac

25

<210> 34

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 34

cctcgactgc agacccctag acacc

25

<210> 35

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 35

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Val Val Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420

<210> 36

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Asp Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420

<210> 37

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 37

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420